

Applicants:
Application No.:
For:
Agent:

Bruce D. Cohen et al.
To Be Assigned
ANTIBODIES TO INSULIN-LIKE GROWTH
FACTOR I RECEPTOR
Karen E. Brown, Reg. No. 43,866 Sheet 1 of 25

Docket No.: ABX-PF2 US

Filed: Herewith

Express Mail No.
EL 889410403 US

2.13.2K	GACATCCAGA	TGACCCAGTT	TCCATCCTCC	CTGTC	TGCAT	CTGTAGGAGA	50
A30	GACATCCAGA	TGACCCAGTC	TCCATCCTCC	CTGTCT	TGCAT	CTGTAGGAGA	50
2.14.3K	-----	-----	---TCCTCC	CTGTCT	TGCAT	CTGTAGGAGA	26
2.12.1K	-----	-----	-----	-----	TGCAT	CTGTAGGAGA	15
4.9.2K	GACATCCAGA	TGACCCAGTC	TCCATCCTCC	CTGTCT	TGCAT	CTGTAGGAGA	50
Consensus	GACATCCAGA	TGACCCAGTV	TCCATCCTCC	CTGTCT	TGCAT	CTGTAGGAGA	50

CDR1

2.13.2K	CAGAGTCACC	ATCACTTGCC	GGGCAAGTCA	GGC	CATTAGA	AATGATTTAG	100
A30	CAGAGTCACC	ATCACTTGCC	GGGCAAGTCA	GGC	CATTAGA	AATGATTTAG	100
2.14.3K	CAGAGTCACC	ATCACTTGCC	GGGCAAGTCA	GGC	CATTAGA	CGTGATTTAG	76
2.12.1K	CAGAGTCACC	ATCACTTGCC	GGGCAAGTCA	GGC	CATTAGA	CGTGATTTAG	65
4.9.2K	CAGAGTCACC	ATCACTTGCC	GGGCAAGTCA	GGC	CATTAGA	ATGATTTAG	100
Consensus	CAGAGTCACC	ATCACTTGCC	GGGCAAGTCA	GGC	CATTAGA	MTGATTTAG	100

2.13.2K	GCTGGTATCA	GCAGAAACCA	GGGAAAGCC	CTAAGCGCCT	GATCTATGCT	150
A30	GCTGGTATCA	GCAGAAACCA	GGGAAAGCC	CTAAGCGCCT	GATCTATGCT	150
2.14.3K	GCTGGTATCA	GCAGAAACCA	GGGAAAGCC	CTAAGCGCCT	GATCTATGCT	126
2.12.1K	GCTGGTATCA	GCAGAAACCA	GGGAAAGCC	CTAAGCGCCT	GATCTATGCT	115
4.9.2K	GCTGGTATCA	GCAGAAACCA	GGGAAAGCC	CTAAGCGCCT	GATCTATGCT	150
Consensus	GCTGGTATCA	GCAGAAACCA	GGGAAAGCC	CTAAGCGCCT	GATCTATGCT	150

CDR2

2.13.2K	GCATCCGTTT	TCCAAAGTGG	GGTCCCACATCA	AGGTTACGCG	GCAGTGGATC	200
A30	GCATCCGTTT	TCCAAAGTGG	GGTCCCACATCA	AGGTTACGCG	GCAGTGGATC	200
2.14.3K	GCATCCGTTT	TCCAAAGTGG	GGTCCCACATCA	AGGTTACGCG	GCAGTGGATC	176
2.12.1K	GCATCCGTTT	TCCAAAGTGG	GGTCCCACATCA	AGGTTACGCG	GCAGTGGATC	165
4.9.2K	GCATCCGTTT	TCCAAAGTGG	GGTCCCACATCA	AGGTTACGCG	GCAGTGGATC	200
Consensus	GCATCCGTTT	TCCAAAGTGG	GGTCCCACATCA	AGGTTACGCG	GCAGTGGATC	200

2.13.2K	TGGGACAGAA	TTCACTCTCA	CAATCAGCAG	CCTGCAGCCT	GAAGATTTTG	250
A30	TGGGACAGAA	TTCACTCTCA	CAATCAGCAG	CCTGCAGCCT	GAAGATTTTG	250
2.14.3K	TGGGACAGAA	TTCACTCTCA	CAATCAGCAG	CCTGCAGCCT	GAAGATTTTG	226
2.12.1K	TGGGACAGAA	TTCACTCTCA	CAATCAGCAG	CCTGCAGCCT	GAAGATTTTG	215
4.9.2K	TGGGACAGAA	TTCACTCTCA	CAATCAGCAG	CCTGCAGCCT	GAAGATTTTG	250
Consensus	TGGGACAGAA	TTCACTCTCA	CAATCAGCAG	CCTGCAGCCT	GAAGATTTTG	250

CDR3

2.13.2K	CAACTTATTA	CTGTCTACAG	CATAATAAGTT	ATCCCTGCAG	TTTGGCCAG	300
A30	CAACTTATTA	CTGTCTACAG	CATAATAAGTT	ATCCCTGCAG	TTTGGCCAG	288
2.14.3K	CAACTTATTA	CTGTCTACAG	CATAATAAGTT	ATCCCTGCAG	TTTGGCCAG	276
2.12.1K	CAACTTATTA	CTGTCTACAG	CATAATAAGTT	ATCCCTGCAG	TTTGGCCAG	265
4.9.2K	CAACTTATTA	CTGTCTACAG	CATAATAAGTT	ATCCCTGCAG	TTTGGCCAG	300
Consensus	CAACTTATTA	CTGTCTACAG	CATAATAAGTT	ATCCCTGCAG	TTTGGCCAG	300

2.13.2K	GGGACCAAGC	TGGAGATCAA	AC----	322
A30	GGGACCAAGC	TGGAGATCAA	AC----	288
2.14.3K	GGGACCAAGC	TGGAGATCAA	ACGAAC	302
2.12.1K	GGGACCAAGC	TGGAGATCAA	ACGAAC	291
4.9.2K	GGGACCAAGC	TGGAGATCAA	AC----	322
Consensus	GGGACCAAGC	TGGAGATCAA	ACGAAC	326

FIG. 1A

4.17.3K	-----	-----	-----	-----	AGGAGA	7
012	GACATCCAGA	TGACCCAGTC	TCCATCCTCC	CTGTCTGCAT	CTGTAGGAGA	50
Consensus	GACATCCAGA	TGACCCAGTC	TCCATCCTCC	CTGTCTGCAT	CTGYAGGAGA	50
CDR1						
4.17.3K	CAGAGTCACC	ATCACTTGCC	GGGCAAGTCA	GAGCATTAGT	ASCTTTTAA	57
012	CAGAGTCACC	ATCACTTGCC	GGGCAAGTCA	GAGCATTAGC	ASCTTTTAA	100
Consensus	CAGAGTCACC	ATCACTTGCC	GGGCAAGTCA	GAGCATTAGY	ASCTTTTAA	100
4.17.3K	ATTGGTATCA	GCAGAAACCA	GGGAAAGCCC	CTAAACTCCT	GATCATGTT	107
012	ATTGGTATCA	GCAGAAACCA	GGGAAAGCCC	CTAAAGCTCCT	GATCATGCT	150
Consensus	ATTGGTATCA	GCAGAAACCA	GGGAAAGCCC	CTAAACTCCT	GATCATGCT	150
CDR2						
4.17.3K	GCATCCAGTT	TGCAGGTGG	GGTCCCATCA	AGGTTCAAGT	GCAGTGGATC	157
012	GCATCCAGTT	TGCAGGTGG	GGTCCCATCA	AGGTTCAAGT	GCAGTGGATC	200
Consensus	GCATCCAGTT	TGCAGGTGG	GGTCCCATCA	AGGTTCAAGT	GCAGTGGATC	200
4.17.3K	TGGGACAGAT	TTCACTCTCA	CCATCAGCAG	TCTGCAACCT	GAAGATTTTG	207
012	TGGGACAGAT	TTCACTCTCA	CCATCAGCAG	TCTGCAACCT	GAAGATTTTG	250
Consensus	TGGGACAGAT	TTCACTCTCA	CCATCAGCAG	TCTGCAACCT	GAAGATTTTG	250
CDR3						
4.17.3K	CAACTTACTA	CTGTCAACAG	AGTTACATG	CCCCACTCAC	TTTCGGCGGA	257
012	CAACTTACTA	CTGTCAACAG	AGTTACATTA	CCCC-TTCH-	-----	288
Consensus	CAACTTACTA	CTGTCAACAG	AGTTACATR	CCCCAYTCH	TTTCGGCGGA	300
4.17.3K	GGGACCAAGG	TGGAGATCAA	AC			279
012	-----	-----	--			288
Consensus	GGGACCAAGG	TGGAGATCAA	AC			322

FIG. 1B

6.1.1K	-----	-----	-----	-----	-----	
A27	GAAATTGTGT	TGACGCAGTC	TCCAGGCACC	CTGTCTTTGT	CTCCAGGGGA	50
Consensus	GAAATTGTGT	TGACGCAGTC	TCCAGGCACC	CTGTCTTTGT	CTCCAGGGGA	50
				CDR1		
6.1.1K	-AGAGCCACC	CTCTCCTGTA	GGGCCAGTCA	GAGTGTTCG	GGCAGCTACT	49
A27	AGAGCCACC	CTCTCCTGTA	GGGCCAGTCA	GAGTGTTCG	AGCAGCTACT	100
Consensus	AGAGCCACC	CTCTCCTGTA	GGGCCAGTCA	GAGTGTTCG	AGCAGCTACT	100
6.1.1K	TAGCCTGGTA	CCAGCAGAAA	CCTGGCCAGG	CTCCCAGGCT	CCTCATCTAT	99
A27	TAGCCTGGTA	CCAGCAGAAA	CCTGGCCAGG	CTCCCAGGCT	CCTCATCTAT	150
Consensus	TAGCCTGGTA	CCAGCAGAAA	CCTGGCCAGG	CTCCCAGGCT	CCTCATCTAT	150
		CDR2				
6.1.1K	GGTGCAATCCA	GCAGGGCCAC	TGGCATCCCA	GACAGGTTCA	GTGGCAGTGG	149
A27	GGTGCAATCCA	GCAGGGCCAC	TGGCATCCCA	GACAGGTTCA	GTGGCAGTGG	200
Consensus	GGTGCAATCCA	GCAGGGCCAC	TGGCATCCCA	GACAGGTTCA	GTGGCAGTGG	200
6.1.1K	GTCTGGGACA	GACTTCACTC	TCACCATCAG	CAGACTGGAG	CCTGAAGATT	199
A27	GTCTGGGACA	GACTTCACTC	TCACCATCAG	CAGACTGGAG	CCTGAAGATT	250
Consensus	GTCTGGGACA	GACTTCACTC	TCACCATCAG	CAGACTGGAG	CCTGAAGATT	250
			CDR3			
6.1.1K	TTTGCAGTGT	TTACTGTCAG	CAGTATGGTA	GTTCACCTCG	NACGTTCCGC	249
A27	TTTGCAGTGT	TTACTGTCAG	CAGTATGGTA	GTTCACCTCG	-----	290
Consensus	TTTGCAGTGT	TTACTGTCAG	CAGTATGGTA	GTTCACCTCG	NACGTTCCGC	300
6.1.1K	CAAGGGACCA	AGGTGGAAAT	CAAAC			274
A27	CAAGGGACCA	AGGTGGAAAT	CAAAC			290
Consensus	CAAGGGACCA	AGGTGGAAAT	CAAAC			325

FIG. 1C

2.12.1.H	-----	-----	---GGGAGGC	TTGGTCAAGC	CTGGA	GGTC	26
DP35	CAGGTGCAGC	TGGTGGAGTC	TGGGGGAGGC	TTGGTCAAGC	CTGGA	GGTC	50
Consensus	CAGGTGCAGC	TGGTGGAGTC	TGGGGGAGGC	TTGGTCAAGC	CTGGA	GGTC	50
						CDR1	
2.12.1.H	CCTGAGACTC	TCCTGTGCAG	CCTCTGGATT	CAC	TTTCAGT	GACTACTATA	76
DP35	CCTGAGACTC	TCCGTGTGCAG	CCTCTGGATT	CAC	TTTCAGT	GACTACTATA	100
Consensus	CCTGAGACTC	TCCGTGTGCAG	CCTCTGGATT	CAC	TTTCAGT	GACTACTATA	100
2.12.1.H	TGAGCTGGAT	CCGCCAGGCT	CCAGGGAAGG	GGCTGGATG	GGTTTCATAC		126
DP35	TGAGCTGGAT	CCGCCAGGCT	CCAGGGAAGG	GGCTGGATG	GGTTTCATAC		150
Consensus	TGAGCTGGAT	CCGCCAGGCT	CCAGGGAAGG	GGCTGGATG	GGTTTCATAC		150
						CDR2	
2.12.1.H	ATTAGTAGTA	GTGGTAGTAC	CAGAACTAC	GCAGACTCTG	TGAAGGGCCG		176
DP35	ATTAGTAGTA	GTGGTAGTAC	CAGAACTAC	GCAGACTCTG	TGAAGGGCCG		200
Consensus	ATTAGTAGTA	GTGGTAGTAC	CAGAACTAC	GCAGACTCTG	TGAAGGGCCG		200
2.12.1.H	ATTACCATC	TCCAGGGACA	ACGCCAAGAA	CTCACTGTAT	CTGCAAATGA		226
DP35	ATTACCATC	TCCAGGGACA	ACGCCAAGAA	CTCACTGTAT	CTGCAAATGA		250
Consensus	ATTACCATC	TCCAGGGACA	ACGCCAAGAA	CTCACTGTAT	CTGCAAATGA		250
2.12.1.H	ACAGCCTGAG	AGCCGAGGAC	ACGCCCGTGT	ATTACTGTCT	GAGAGATGGA		276
DP35	ACAGCCTGAG	AGCCGAGGAC	ACGCCCGTGT	ATTACTGTCT	GAGAGATGGA		296
Consensus	ACAGCCTGAG	AGCCGAGGAC	ACGCCCGTGT	ATTACTGTCT	GAGAGATGGA		300
						CDR3	
2.12.1.H	GTGGAACCTA	CTTTTACTA	CTACTACTAC	GGTATGGACG	TCTGGGGCCA		326
DP35	GTGGAACCTA	CTTTTACTA	CTACTACTAC	GGTATGGACG	TCTGGGGCCA		296
Consensus	GTGGAACCTA	CTTTTACTA	CTACTACTAC	GGTATGGACG	TCTGGGGCCA		350
2.12.1.H	AGGGACCACG	GTCACCGTCT	CCTCAG				352
DP35	AGGGACCACG	GTCACCGTCT	CCTCAG				296
Consensus	AGGGACCACG	GTCACCGTCT	CCTCAG				376

FIG. 2A

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PF2-2.14.3H.DNA	-----	GGGCCCAGGA	CTGGTGAAGC	CTTCGGAGAC	30
VIV-4/4.35	CAGGTGCAGC	TGCAGGAGTC	GGGCCCAGGA	CTGGTGAAGC	50
Consensus	CAGGTGCAGC	TGCAGGAGTC	GGGCCCAGGA	CTTCGGAGAC	50
				CDR1	
PF2-2.14.3H.DNA	CCTGTCCCTC	ACCTGCACGT	TCTCTGGTGG	CTCCATCAGT	80
VIV-4/4.35	CCTGTCCCTC	ACCTGCACGT	TCTCTGGTGG	CTCCATCAGT	100
Consensus	CCTGTCCCTC	ACCTGCACGT	TCTCTGGTGG	CTCCATCAGT	100
				CDR1	
PF2-2.14.3H.DNA	GGAGCTGGAT	CCGGCAGCCC	GCCGGGAAGG	GACTGGAGTG	130
VIV-4/4.35	GGAGCTGGAT	CCGGCAGCCC	GCCGGGAAGG	GACTGGAGTG	150
Consensus	GGAGCTGGAT	CCGGCAGCCC	GCCGGGAAGG	GACTGGAGTG	150
				CDR2	
PF2-2.14.3H.DNA	ATCTATACCA	GTGGGAGGAC	CAACTACAAC	CCCTCCCTCA	180
VIV-4/4.35	ATCTATACCA	GTGGGAGGAC	CAACTACAAC	CCCTCCCTCA	200
Consensus	ATCTATACCA	GTGGGAGGAC	CAACTACAAC	CCCTCCCTCA	200
PF2-2.14.3H.DNA	CACCATGTCA	GTAGACACGT	CCAAGAACCA	GTTCCTCCCTG	230
VIV-4/4.35	CACCATGTCA	GTAGACACGT	CCAAGAACCA	GTTCCTCCCTG	250
Consensus	CACCATGTCA	GTAGACACGT	CCAAGAACCA	GTTCCTCCCTG	250
PF2-2.14.3H.DNA	CTGTGACCGC	CGCGGACACG	GCCGTGTATT	ACTGTGCGGT	280
VIV-4/4.35	CTGTGACCGC	CGCGGACACG	GCCGTGTATT	ACTGTGCGGT	288
Consensus	CTGTGACCGC	CGCGGACACG	GCCGTGTATT	ACTGTGCGGT	300
				CDR3	
PF2-2.14.3H.DNA	GGAGTGGTTA	TTATCTTTGA	CTACTGGGGC	CAGGAGACCC	330
VIV-4/4.35	GGAGTGGTTA	TTATCTTTGA	CTACTGGGGC	CAGGAGACCC	294
Consensus	GGAGTGGTTA	TTATCTTTGA	CTACTGGGGC	CAGGAGACCC	350
PF2-2.14.3H.DNA	CTCCTCAG				338
VIV-4/4.35	CTCCTCAG				294
Consensus	CTCCTCAG				358

FIG. 2B

6.1.1.H	GAGGTGCAGC	TGTTGGAGTC	TGGGGGAGGC	TTGGTACAGC	CTGGGGGGGTC	50
4.9.2H	GAGGTGCAGC	TGTTGGAGTC	TGGGGGAGGC	TTGGTACAGC	CTGGGGGGGTC	50
DP47	GAGGTGCAGC	TGTTGGAGTC	TGGGGGAGGC	TTGGTACAGC	CTGGGGGGGTC	50
2.13.2H	GAGGTGCAGC	TGTTGGAGTC	TGGGGGAGGC	TTGGTACAGC	CTGGGGGGGTC	50
Consensus	GAGGTGCAGC	TGTTGGAGTC	TGGGGGAGGC	TTGGTACAGC	CTGGGGGGGTC	50
CDR1						
6.1.1H	CCTGAGACTC	TCCTGTTCAG	CCTCTGGATT	CACCTTTAGC	AGCTATGCCA	100
4.9.2H	CCTGAGACTC	TCCTGTTCAG	CCTCTGGATT	CACCTTTAGC	AGCTATGCCA	100
DP47	CCTGAGACTC	TCCTGTTCAG	CCTCTGGATT	CACCTTTAGC	AGCTATGCCA	100
2.13.2H	CCTGAGACTC	TCCTGTTCAG	CCTCTGGATT	CACCTTTAGC	AGCTATGCCA	100
Consensus	CCTGAGACTC	TCCTGTTCAG	CCTCTGGATT	CACCTTTAGC	AGCTATGCCA	100
CDR2						
6.1.1H	TGAGCTGGGT	CCGCCAGGCT	CCAGGGAAGG	GGCTGGAGTG	GGTCTCAGCT	150
4.9.2H	TGAGCTGGGT	CCGCCAGGCT	CCAGGGAAGG	GGCTGGAGTG	GGTCTCAGCT	150
DP47	TGAGCTGGGT	CCGCCAGGCT	CCAGGGAAGG	GGCTGGAGTG	GGTCTCAGCT	150
2.13.2H	TGAGCTGGGT	CCGCCAGGCT	CCAGGGAAGG	GGCTGGAGTG	GGTCTCAGCT	150
Consensus	TGAGCTGGGT	CCGCCAGGCT	CCAGGGAAGG	GGCTGGAGTG	GGTCTCAGCT	150
CDR2						
6.1.1H	ATTACTGGGA	GTGGTGSTAG	TACATCTAC	GCAGACTCCG	TGAAGGGCCG	200
4.9.2H	ATTACTGGGA	GTGGTGSTAG	TACATCTAC	GCAGACTCCG	TGAAGGGCCG	200
DP47	ATTACTGGGA	GTGGTGSTAG	TACATCTAC	GCAGACTCCG	TGAAGGGCCG	200
2.13.2H	ATTACTGGGA	GTGGTGSTAG	TACATCTAC	GCAGACTCCG	TGAAGGGCCG	200
Consensus	ATTACTGGGA	GTGGTGSTAG	TACATCTAC	GCAGACTCCG	TGAAGGGCCG	200
CDR3						
6.1.1H	GTTCACCATC	TCCAGAGACA	ATTCCAGGAA	CACGCTGTAT	CTGCAAAATGA	250
4.9.2H	GTTCACCATC	TCCAGAGACA	ATTCCAGGAA	CACGCTGTAT	CTGCAAAATGA	250
DP47	GTTCACCATC	TCCAGAGACA	ATTCCAGGAA	CACGCTGTAT	CTGCAAAATGA	250
2.13.2H	GTTCACCATC	TCCAGAGACA	ATTCCAGGAA	CACGCTGTAT	CTGCAAAATGA	250
Consensus	GTTCACCATC	TCCAGAGACA	ATTCCAGGAA	CACGCTGTAT	CTGCAAAATGA	250
CDR3						
6.1.1H	ACAGCCTGAG	AGCCGAGGAC	ACGGCCGTAT	ATTACTGTGC	GAAGAATCTC	298
4.9.2H	ACAGCCTGAG	AGCCGAGGAC	ACGGCCGTAT	ATTACTGTGC	GAAGAATCTC	300
DP47	ACAGCCTGAG	AGCCGAGGAC	ACGGCCGTAT	ATTACTGTGC	GAAGAATCTC	296
2.13.2H	ACAGCCTGAG	AGCCGAGGAC	ACGGCCGTAT	ATTACTGTGC	GAAGAATCTC	300
Consensus	ACAGCCTGAG	AGCCGAGGAC	ACGGCCGTAT	ATTACTGTGC	GAAGAATCTC	300
CDR3-for 4.9.2 and 2.13.2						
6.1.1H	-----	-----	-----	-----	C-----	299
4.9.2H	GGCTACGGTG	ACTTTTACTA	CTACTACTAC	GGTATGGACG	TCTGGGGCCA	350
DP47	-----	-----	-----	-----	-----	296
2.13.2H	GGCTGTGCCG	ACTCTTACTA	CTACTACTAC	GGTATGGACG	TCTGGGGCCA	350
Consensus	GGCTRSKSYG	ACTYTTACTA	CTACTACTAC	GGTATGGACG	TCTGGGGCCA	350
CDR3-for 6.1.1						
6.1.1H	AGGGACTACG	GTGATTATGA	GTTGGTTTCGA	CCCCTGGGGC	CAGGGAACCC	349
4.9.2H	AGGGACCAC-	-----	-----	-----	-----	359
DP47	-----	-----	-----	-----	-----	296
2.13.2H	AGGGACCAC-	-----	-----	-----	-----	359
Consensus	AGGGACYACG	GTGATTATGA	GTTGGTTTCGA	CCCCTGGGGC	CAGGGAACCC	400

FIG. 2C-1

6.1.1.H	TGGTCACCGT CTCCTCAG	367
4.9.2.H	-GGTCACCGT CTCCTCAG	376
DP47	-----	296
2.13.2.H	-GGTCACCGT CTCCTCAG	376
Consensus	TGGTCACCGT CTCCTCAG	418

FIG. 2C-2

4.17.3H	-----	-----	---CCGAGGA	CTGGTGAAGC	CTTCGGAGAC	27
DP71	CAGGTGCAGC	TGCAGGAGTC	GGGCCAGGA	CTGGTGAAGC	CTTCGGAGAC	50
Consensus	CAGGTGCAGC	TGCAGGAGTC	GGGCCAGGA	CTGGTGAAGC	CTTCGGAGAC	50
CDR1						
4.17.3H	CCTGTCCCTC	ACCTGCACTG	TCTCTGGTGG	CTCCATCAGT	AGTTACTACT	77
DP71	CCTGTCCCTC	ACCTGCACTG	TCTCTGGTGG	CTCCATCAGT	AGTTACTACT	100
Consensus	CCTGTCCCTC	ACCTGCACTG	TCTCTGGTGG	CTCCATCAGT	AGTTACTACT	100
CDR1						
4.17.3H	GGAGTTGGAT	CCGGCAGCCC	CCAGGGAAGG	GACTGGAGTG	GATTGGGTAT	127
DP71	GGAGCTGGAT	CCGGCAGCCC	CCAGGGAAGG	GACTGGAGTG	GATTGGGTAT	150
Consensus	GGAGTTGGAT	CCGGCAGCCC	CCAGGGAAGG	GACTGGAGTG	GATTGGGTAT	150
CDR2						
4.17.3H	ATCTATTACA	GTGGGAGCAC	CAACTACAAC	CCCTCCCTCA	AGAGTCGAGT	177
DP71	ATCTATTACA	GTGGGAGCAC	CAACTACAAC	CCCTCCCTCA	AGAGTCGAGT	200
Consensus	ATCTATTACA	GTGGGAGCAC	CAACTACAAC	CCCTCCCTCA	AGAGTCGAGT	200
CDR3						
4.17.3H	CACCATATCA	GTAGACACGT	CCAAGAACCA	GTTCTCCCTG	AAGCTGAGCT	227
DP71	CACCATATCA	GTAGACACGT	CCAAGAACCA	GTTCTCCCTG	AAGCTGAGCT	250
Consensus	CACCATATCA	GTAGACACGT	CCAAGAACCA	GTTCTCCCTG	AAGCTGAGCT	250
CDR3						
4.17.3H	CTGTGACCGC	TGCGGACACG	GCCGTGTATT	ACTGTGCCAG	GACGTATAGC	277
DP71	CTGTGACCGC	TGCGGACACG	GCCGTGTATT	ACTGTGCCAG	GA-----	289
Consensus	CTGTGACCGC	TGCGGACACG	GCCGTGTATT	ACTGTGCCAG	GACGTATAGC	300
CDR3						
4.17.3H	AGTTCGTCTC	ACTACTACGG	TATGACGTC	TGGGGCCAAG	GAACACGGT	327
DP71	-----	-----	GA-----	-----	GA-----	293
Consensus	AGTTCGTCTC	ACTACTACGG	TATGACGTC	TGGGGCCAAG	GAACACGGT	350
CDR3						
4.17.3H	CACCGTCTCC	TCAG				341
DP71	-----	-----				293
Consensus	CACCGTCTCC	TCAG				364

FIG. 2D

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Sheet 8 of 25

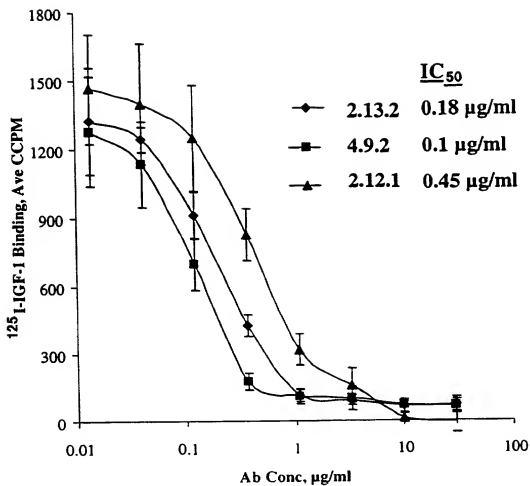


FIG. 3

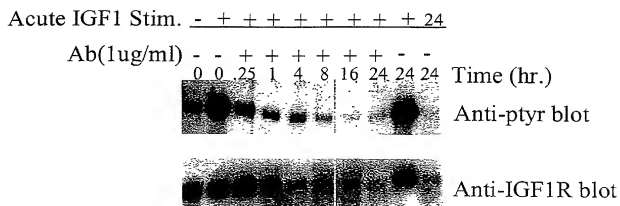


FIG. 4

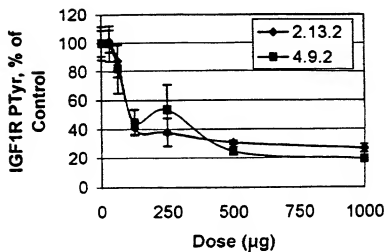


FIG. 5

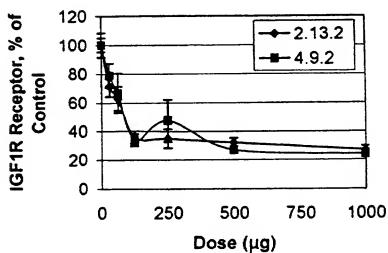
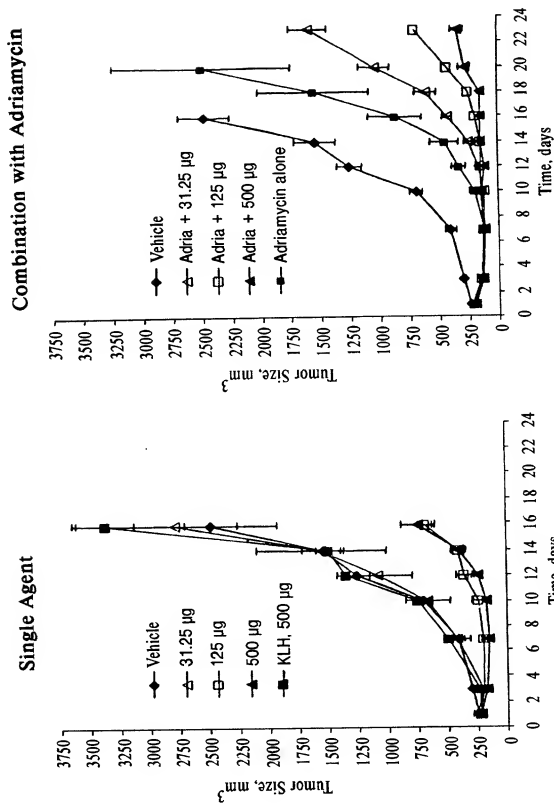


FIG. 6



Treatment: 125 μ g dose

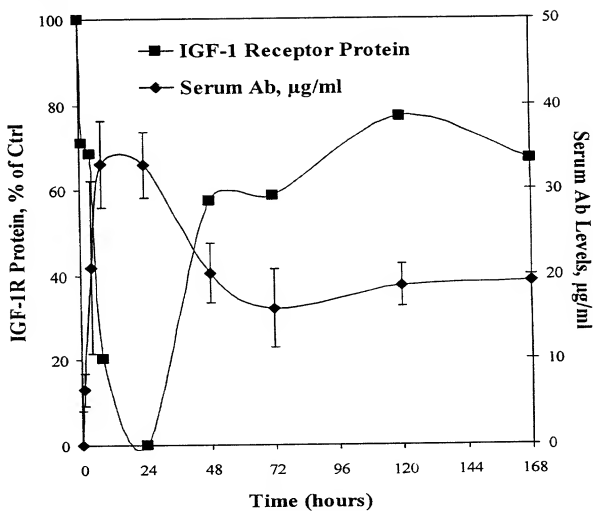


FIG. 8

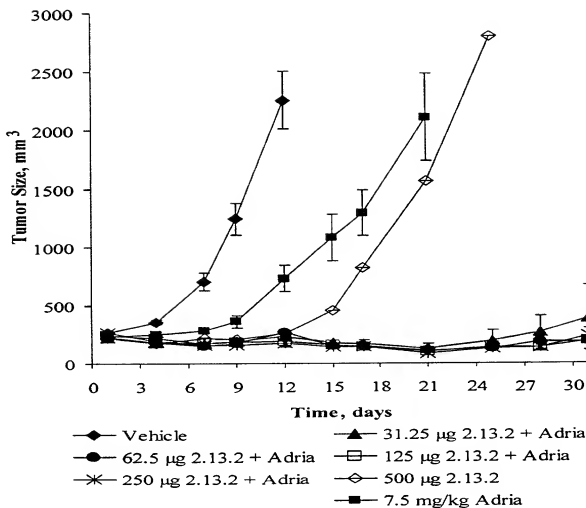


FIG. 9

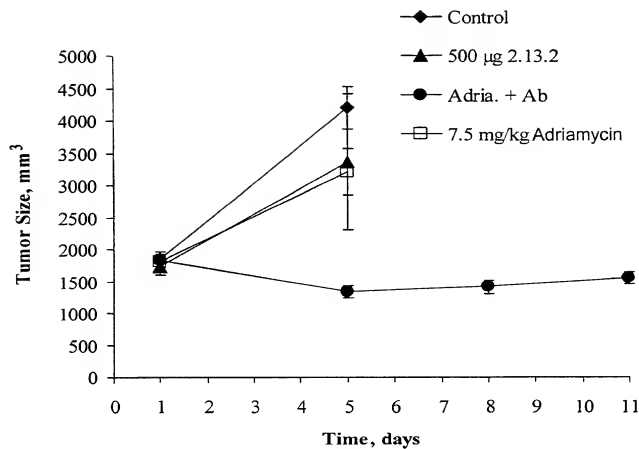
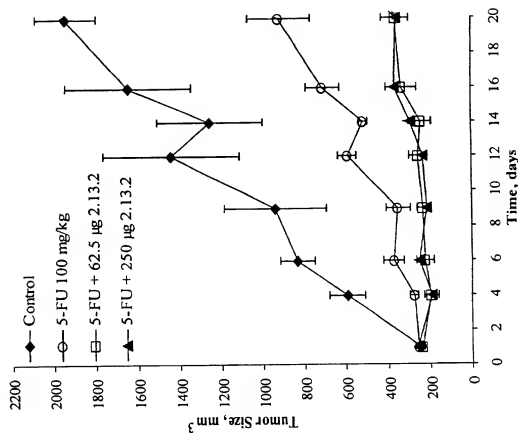


FIG. 10

Combination



Single Agent

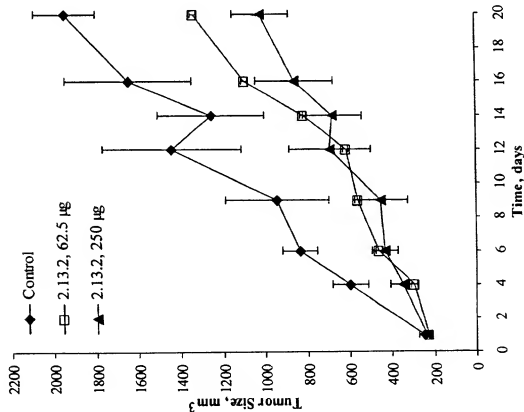


FIG. 11

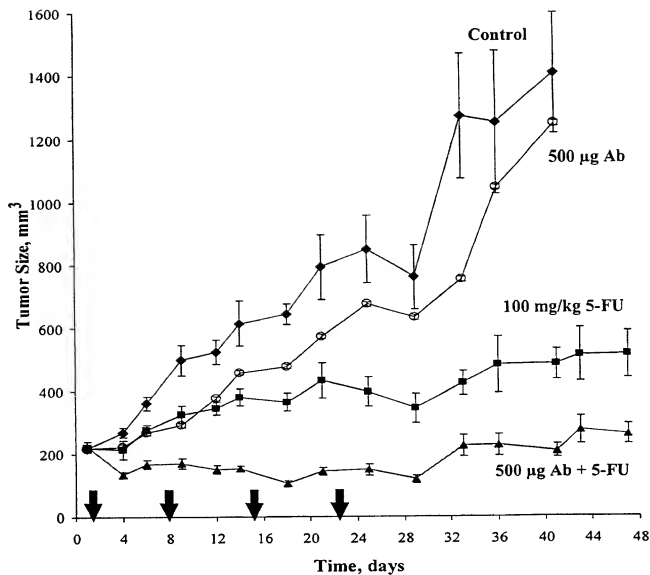


FIG. 12

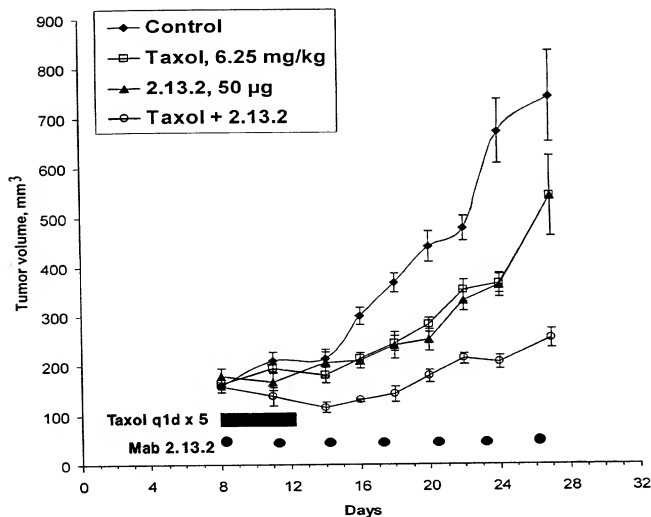
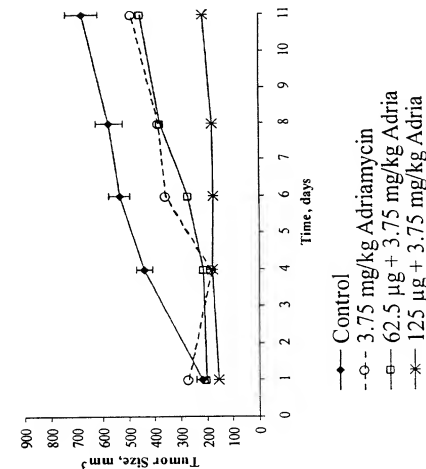


FIG. 13

Combination



Single Agent

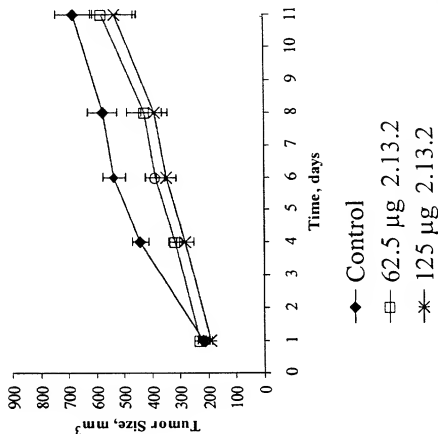


FIG. 14

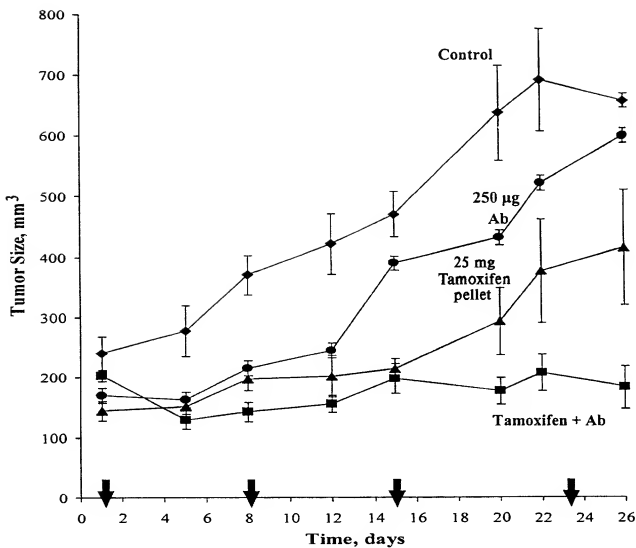


FIG. 15

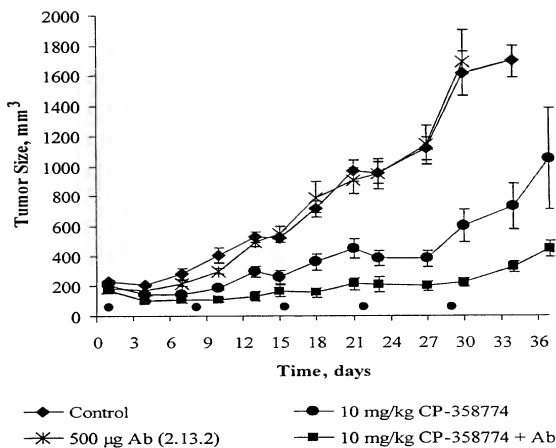


FIG. 16

Applicants:
Application No.:
For:
Agent:

Bruce D. Cohen et al.
To Be Assigned
ANTIBODIES TO INSULIN-LIKE GROWTH
FACTOR I RECEPTOR
Karen E. Brown, Reg. No. 43,866

Docket No.: ABX-PF2 US
Filed: Herewith
Sheet 21 of 25

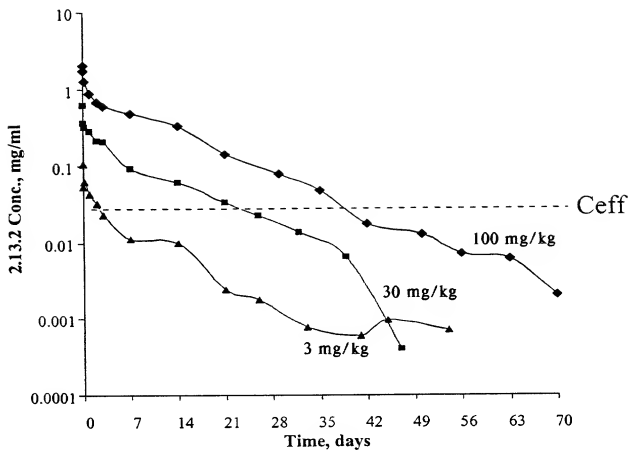


FIG. 17

Applicants:
Application No.:
For:

Agent:

Bruce D. Cohen et al.
To Be Assigned
ANTIBODIES TO INSULIN-LIKE GROWTH
FACTOR I RECEPTOR
Karen E. Brown, Reg. No. 43,866

Docket No.: ABX-PF2 US
Filed: Herewith

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	Control Tumors	Treated Tumors
2.13.2 Treated		
Adriamycin Treated		
2.13.2 + Adriamycin Treated		

FIG. 18

Clone	C domain mutations	FR mutation	CDR mutation	Change in Cys	Change in glycosylation
2.13.2 Heavy	0	3	8	0	0
2.13.2 Light	0	1	4	1 (CDR3)	0
2.12.2 Heavy	0	2	8	0	0
2.12.2 Light	0	3	5	0	0

FIG. 19A

PF2 2.13.2 Heavy chain (DP-47(3-23)/D6-19/JH6) +

NEFGLSWLFL VAILKGVOCE VQLLESGGGL VQPGSLRLS CTASGTFSS YAMNVRQAP GKGLEWWSAI SGGSGTFFYA DSVIGRFTIS RDNSRTTLYL ++
 NEFGLSWLFL VAILKGVOCE VQLLESGGGL VQPGSLRLS CAASGTFSS YAMNVRQAP GKGLEWWSAI SGGSGTFFYA DSVIGRFTIS RDNSKNTLLH * *
 QNLSRAEDT AVTYCAK--D LGWSDSYIYY YGNDVWGQGT TWTVSSASTK GPSVFPLAPC SRSTSESTAA LGCLVKDYFP EPTVSWNSG ALTSGVHTFP
 QNLSRAEDT AVTYCAKGIS SGW--YIYY YGNDVWGQGT TWTVSSASTK GPSVFPLAPC SRSTSESTAA LGCLVKDYFP EPTVSWNSG ALTSGVHTFP * * * *
 AVLOSSGLYS LSSVTVTPSS NFGTQTYTCN VDHKPSNTKV DKTVERKCCV ECPPCPAPV AGPSVFLPPP KPQDTLMISR TPEVTCVVVD VSHEDPEVQF
 AVLOSSGLYS LSSVTVTPSS NFGTQTYTCN VDHKPSNTKV DKTVERKCCV ECPPCPAPV AGPSVFLPPP KPQDTLMISR TPEVTCVVVD VSHEDPEVQF
 NWYDGVGVH NAKTKPREQ FNSTFRVSV LTVWHDWLN GREYKCKVSN KGLPAPIENT ISKTKQPRE PQVYTLPPSR EEMTKNQVSL TCLVKGFYPS
 NWYDGVGVH NAKTKPREQ FNSTFRVSV LTVWHDWLN GREYKCKVSN KGLPAPIENT ISKTKQPRE PQVYTLPPSR EEMTKNQVSL TCLVKGFYPS
 DIAVWESNG QPENNYKTP PMLDSGSGFF LYSKLTVDKS RMOQGNVFC SVWHEALHNN YTKSLSLSP GK
 DIAVWESNG QPENNYKTP PMLDSGSGFF LYSKLTVDKS RMOQGNVFC SVWHEALHNN YTKSLSLSP GK

FIG. 19B

FIG. 19C

[illegible]

FIG. 19D

For:

To Be Assigned

Filed: Herewith

ANTIBODIES TO INSULIN-LIKE GROWTH

Agent:

FACTOR I RECEPTOR

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PF2.12.1 Light chain (A30/Jk1)

$\begin{array}{ccccccc} \text{MDMVRVPAQLL} & \text{GLLLLPFQA} & \text{RCDIQWTSQ} & \text{SLSIASVGDR} & \text{VFTRCRASQ} & \text{IRDLGWYQQ} & \text{KPGKAPRLI} \\ * & + & & & & & \\ \text{MDMVRVPAQLL} & \text{GLLLLPFQA} & \text{RCDIQWTSQ} & \text{SLSIASVGDR} & \text{VFTRCRASQ} & \text{IRDLGWYQQ} & \text{KPGKAPRLI} \\ * & + & & & & & \\ \text{QPEDPFIATYC} & \text{LOHNPTPT} & \text{GQTVEILIR} & \text{TVAASVPFI} & \text{PPSDQELKSG} & \text{TASVVCLLN} & \text{FYPREAKOV} \\ * & + & & & & & \\ \text{QPEDPFIATYC} & \text{LOHNSPIFI} & \text{GQTKVEIKR} & \text{TVAASVPFI} & \text{PPSDQELKSG} & \text{TASVVCLLN} & \text{FYPREAKOV} \\ & & & & & & \\ \text{LTLSKADYEK} & \text{HKVACEVTH} & \text{QGSSSPVTKS} & \text{FNREGC} & & & \\ & & & & & & \\ \text{LTLSKADYEK} & \text{HKVACEVTH} & \text{QGSSSPVTKS} & \text{FNREGC} & & & \end{array}$

FIG. 19E